



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,499

DATE: 06/19/2003
TIME: 16:02:29

Input Set : A:\4085-226-27.ST25.txt
Output Set: N:\CRF4\06192003\I654499.raw

3 <110> APPLICANT: Palmer, Michelle A.J.
 4 Gee, Melissa
 5 Tillotson, Bonnie
 6 Chang, Xiao-Jia
 8 <120> TITLE OF INVENTION: Receptor Function Assay for G-Protein Coupled Receptors and
 Orphan
 9 Receptors by Reporter Enzyme Mutant Complementation
 11 <130> FILE REFERENCE: 4085-226-27
 13 <140> CURRENT APPLICATION NUMBER: US 09/654,499
 14 <141> CURRENT FILING DATE: 2000-09-01
 16 <150> PRIOR APPLICATION NUMBER: US 60/180,669
 17 <151> PRIOR FILING DATE: 2000-02-07
 19 <160> NUMBER OF SEQ ID NOS: 6
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 6700
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Nucleotide sequence for pICAST ALC
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 32 <222> LOCATION: (1457)...(4486)
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 36 gggccaagaa cagatggAAC agctgaatat gggccaaaca ggatatactgt ggtaAGCAGT 120
 37 tcctgccccg gctcaggccc aagaacagat ggtccccaga tgcggtccag ccctcagcag 180
 38 tttcttagaga accatcagat gtttccaggg tgcccaagg acctgaaatg accctgtgcc 240
 39 ttatttgaac taaccaatca gttcgcttct cgcttctgtt cgccgcgttc tgctccccga 300
 40 gctcaataaaa agagccaca acccctcaact cggggcgcca gtcctccgat tgactgagtc 360
 41 gcccgggtac ccgtgtatcc aataaaaccct cttgcagttt catccgactt gtggtctcgc 420
 42 tggcccttgg gagggtctcc tctgagtgtat tgactacccg tcagcggggg tctttcattt 480
 43 gggggctcgt ccgggatcgg gagacccctg cccaggacc accgaccac cacccggagg 540
 44 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttt 600
 45 tgcgcctgctcg tggtaact ttagctaact agctctgtat ctggcggacc cgtggggaa 660
 46 ctgacgagtt ctgaacaccc gggcgcaacc ctggagacg tcccaggac tttggggcc 720
 47 gttttgtgg cccgacctga ggaaggggagt cgatgtggaa tccgaccccg tcaggatatg 780
 48 tggttctggt aggagacgag aacctaAAAAC agttcccgcc tccgtctgaa ttttgcttt 840
 49 cggtttgaa ccgaagccgc gcgttctgtc tgctcagca tcgttctgtg ttgtctctgt 900
 50 ctgactgtgt ttctgtatTTT-gtctgaaaaat-taggggcaga-ctgttaaaaae-teeetttaaat-960
 51 ttgaccttag gtaactggaa agatgtcgag cggctcgctc acaaccagtc ggttagatgtc 1020
 52 aagaagagac gttgggttac cttctgtctgc cagaatggc caacctttaa cgtcggtatgg 1080
 53 cccgcgagacg gcacacccaa ccgagacccctc atcaccagg ttaagatcaa ggtctttca 1140
 54 cctggccgcg atggacacccc agaccaggTC ccctacatcg tgacctggaa agcctggct 1200
 55 ttggacccccc ctccctgggt caagccctt gtacacccta agcctccgccc tcctttccct 1260

ENTERED

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56	ccatccgccc	cgtctctccc	ccttgaacct	cctcggtcga	ccccgcctcg	atcctccctt	1320
57	tatccagccc	tcactccttc	tctaggcgcc	ggccgctcta	gcccattaaat	acgactcaact	1380
58	atagggcgat	tcgaatcagg	ccttggcgcg	ccggatcctt	aattaagcgc	aattgggagg	1440
59	tggcggttagc	ctcgag	atg ggc	gtg att acg	gat tca ctg	gcc gtc gtg	gcc 1492
60	Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala						
61	1	5	10				
63	cgc acc gat cgc	cct tcc	caa cag	tta cgc	agc ctg	aat ggc gaa	tgg 1540
64	Arg Thr Asp Arg Pro Ser Gln	Gln Leu Arg Ser Leu Asn	Gly Glu Trp				
65	15	20	25				
67	cgc ttt gcc tgg ttt ccg	gca cca	gaa gcg	gtg ccg	gaa agc	tgg ctg	1588
68	Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro	Glu Ser Trp	Leu				
69	30	35	40				
71	gag tgc gat ctt cct	gag gcc	gat act	gtc gtc	ccc tca	aac tgg	1636
72	Glu Cys Asp Leu Pro Glu Ala Asp	Thr Val Val Val	Pro Ser Asn Trp				
73	45	50	55	60			
75	cag atg cac ggt tac	gat gct	ccc atc	tac acc	aac gtc	acc tat ccc	1684
76	Gln Met His Gly Tyr Asp Ala Pro Ile Tyr	Thr Asn Val	Thr Tyr Pro				
77	65	70	75				
79	att acg gtc aat ccg	ccg ttt	gtt ccc	acg gag	aat ccg	acg ggt	tgt 1732
80	Ile Thr Val Asn Pro Pro Phe Val Pro	Thr Glu Asn Pro	Thr Gly Cys				
81	80	85	90				
83	tac tcg ctc aca ttt aat	gtt gat	gaa agc	tgg cta	cag gaa	ggc cag	1780
84	Tyr Ser Leu Thr Phe Asn Val Asp	Glu Ser Trp	Leu Gln Glu Gly Gln				
85	95	100	105				
87	acg cga att att ttt	gat ggc	gtt aac	tcg gcg	ttt cat	ctg tgg	tgc 1828
88	Thr Arg Ile Ile Phe Asp	Gly Val Asn Ser	Ala Phe His Leu Trp Cys				
89	110	115	120				
91	aac ggg cgc tgg gtc	ggt tac	ggc cag	gac agt	cgt ttg	ccg tct	gaa 1876
92	Asn Gly Arg Trp Val	Gly Tyr Gly Gln Asp	Ser Arg Leu Pro Ser	Glu			
93	125	130	135	140			
95	ttt gac ctg	agc gca	ttt tta	cgc gcc	gga gaa	aac cgc	ctc gcg 1924
96	Phe Asp Leu Ser Ala	Phe Leu Arg Ala	Gly Glu Asn Arg	Leu Ala Val			
97	145	150	155				
99	atg gtg ctg cgc tgg	agt gac	ggc agt	tat ctg	gaa gat	cag gat	atg 1972
100	Met Val Leu Arg Trp Ser Asp	Gly Ser Tyr	Leu Glu Asp	Gln Asp Met			
101	160	165	170				
103	tgg cgg atg agc	ggc att	tcc cgt	gac gtc	ttg ctg	cat aaa ccg	2020
104	Trp Arg Met Ser	Gly Ile Phe Arg Asp	Val Ser Leu	Leu His Lys Pro			
105	175	180	185				
107	act aca caa atc	agc gat	tcc cat	gtt gcc	act cgc	ttt aat	gat gat 2068
108	Thr Thr Gln Ile Ser Asp	Phe His Val	Ala Thr Arg	Phe Asn Asp			
109	190	195	200				
111	ttc agc cgc	gct gta	ctg gag	gct gaa	gtt cag	atg tgc	ggc gag ttg 2116
112	Phe Ser Arg Ala Val	Leu Glu Ala Glu	Val Gln Met	Cys Gly Glu	Leu		
113	205	210	215	220			
115	cgt gac tac cta	cggt gta	aca gtt	tct tta	tgg cag	ggt gaa	acg cag 2164
116	Arg Asp Tyr Leu Arg Val	Thr Val Ser	Leu Trp Gln	Gly Glu	Thr Gln		
117	225	230	235				
119	gtc gcc agc	ggc acc	gct ttc	ggc ggt	gaa att	atc gat	gag cgt 2212

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120 Val Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg		
121 240	245	250
123 ggt ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg		2260
124 Gly Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro		
125 255	260	265
127 aaa ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa		2308
128 Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu		
129 270	275	280
131 ctg cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc		2356
132 Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val		
133 285	290	295
135 ggt ttc cgc gag gtg cgg att gaa aat ggt ctg ctg ctg aac ggc		2404
136 Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Asn Gly		
137 305	310	315
139 aag ccg ttg ctg att cga ggc gtt aac cgt cac gag cat cat cct ctg		2452
140 Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu		
141 320	325	330
143 cat ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg		2500
144 His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu		
145 335	340	345
147 atg aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac		2548
148 Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn		
149 350	355	360
151 cat ccg ctg tgg tac acg ctg tgc gac cgc tac ggc ctg tat gtg gtg		2596
152 His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val		
153 365	370	375
155 gat gaa gcc aat att gaa acc cac ggc atg gtg cca atg aat cgt ctg		2644
156 Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu		
157 385	390	395
159 acc gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga		2692
160 Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg		
161 400	405	410
163 atg gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg		2740
164 Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu		
165 415	420	425
167 ggg aat gaa tca ggc cac ggc gct aat cac gac gcg ctg tat cgc tgg		2788
168 Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp		
169 430	435	440
171 atc aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa ggc ggc gga		2836
172 Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly		
173 445	450	455
175 gcc gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg		2884
176 Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val		
177 465	470	475
179 gat gaa gac cag ccc ttc ccg gct gtg ccg aaa tgg tcc atc aaa aaa		2932
180 Asp Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys		
181 480	485	490
183 tgg ctt tcg cta cct gga gag acg cgc ccg ctg atc ctt tgc gaa tac		2980
184 Trp Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr		

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185	495	500	505	
187	gcc cac gcg atg ggt aac agt ctt ggc ggt ttc gct aaa tac tgg cag			3028
188	Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln			
189	510	515	520	
191	gcg ttt cgt cag tat ccc cgt tta cag ggc ggc ttc gtc tgg gac tgg			3076
192	Ala Phe Arg Gln Tyr Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp			
193	525	530	535	540
195	gtg gat cag tcg ctg att aaa tat gat gaa aac ggc aac ccg tgg tcg			3124
196	Val Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser			
197	545	550	555	
199	gct tac ggc ggt gat ttt ggc gat acg ccg aac gat cgc cag ttc tgt			3172
200	Ala Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys			
201	560	565	570	
203	atg aac ggt ctg gtc ttt gcc gac ccg acg ccg cat cca gcg ctg acg			3220
204	Met Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr			
205	575	580	585	
207	gaa gca aaa cac cag cag cag ttt ttc cag ttc cgt tta tcc ggg caa			3268
208	Glu Ala Lys His Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln			
209	590	595	600	
211	acc atc gaa gtg acc agc gaa tac ctg ttc cgt cat agc gat aac gag			3316
212	Thr Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu			
213	605	610	615	620
215	ctc ctg cac tgg atg gtg gcg ctg gat ggt aag ccg ctg gca agc ggt			3364
216	Leu Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly			
217	625	630	635	
219	gaa gtg cct ctg gat gtc gct cca caa ggt aaa cag ttg att gaa ctg			3412
220	Glu Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu			
221	640	645	650	
223	cct gaa cta ccg cag ccg gag agc gcc ggg caa ctc tgg ctc aca gta			3460
224	Pro Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val			
225	655	660	665	
227	cgc gta gtg caa ccg aac gcg acc gca tgg tca gaa gcc ggg cac atc			3508
228	Arg Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile			
229	670	675	680	
231	agc gcc tgg cag cag tgg cgt ctg gcg gaa aac ctc agt gtg acg ctc			3556
232	Ser Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu			
233	685	690	695	700
235	ccc gcc gcg tcc cac gcc atc ccg cat ctg acc acc agc gaa atg gat			3604
236	Pro Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp			
237	705	710	715	
239	ttt tgc atc gag ctg ggt aat aag cgt tgg caa ttt aac ccg cag tca			3652
240	Phe Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser			
241	720	725	730	
243	ggc ttt ctt tca cag atg tgg att ggc gat aaa aaa caa ctg ctg acg			3700
244	Gly Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr			
245	735	740	745	
247	ccg ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc			3748
248	Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly			
249	750	755	760	

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251	gta	agt	gaa	gcg	acc	cgc	att	gac	cct	aac	gcc	tgg	gtc	gaa	cgc	tgg	3796	
252	Val	Ser	Glu	Ala	Thr	Arg	Ile	Asp	Pro	Asn	Ala	Trp	Val	Glu	Arg	Trp		
253	765				770					775						780		
255	aag	gcg	gca	ggc	cat	tac	cag	gcc	gaa	gca	gca	gca	ttg	ttg	cag	tgc	3844	
256	Lys	Ala	Ala	Gly	His	Tyr	Gln	Ala	Glu	Ala	Ala	Leu	Leu	Gln	Cys	Thr		
257					785					790						795		
259	gca	gat	aca	ctt	gct	gat	gct	gtg	ctg	att	acg	acc	gct	cac	gct	tgg	3892	
260	Ala	Asp	Thr	Leu	Ala	Asp	Ala	Val	Leu	Ile	Thr	Thr	Ala	His	Ala	Trp		
261					800				805							810		
263	cag	cat	cag	ggg	aaa	acc	tta	ttt	atc	agc	cgg	aaa	acc	tac	cgg	att	3940	
264	Gln	His	Gln	Gly	Lys	Thr	Leu	Phe	Ile	Ser	Arg	Lys	Thr	Tyr	Arg	Ile		
265					815				820							825		
267	gat	ggt	agt	ggt	caa	atg	gct	att	acc	gtt	gat	gtt	gaa	gtg	gct	agc	3988	
268	Asp	Gly	Ser	Gly	Gln	Met	Ala	Ile	Thr	Val	Asp	Val	Glu	Val	Ala	Ser		
269					830				835							840		
271	gat	aca	ccg	cat	ccg	gct	cggt	att	ggc	ctg	aat	tgc	cag	ctg	gct	cag	4036	
272	Asp	Thr	Pro	His	Pro	Ala	Arg	Ile	Gly	Leu	Asn	Cys	Gln	Leu	Ala	Gln		
273	845					850					855						860	
275	gta	gca	gag	cggt	gtt	ttt	gca	ttt	ggg	ccg	caa	gaa	aac	tat			4084	
276	Val	Ala	Glu	Arg	Val	Asn	Trp	Leu	Gly	Leu	Gly	Pro	Gln	Glu	Asn	Tyr		
277					865				870							875		
279	ccc	gac	cgct	act	gcc	gcc	tgt	ttt	gac	cgc	tgg	gat	ctg	cca	ttt		4132	
280	Pro	Asp	Arg	Leu	Thr	Ala	Ala	Cys	Phe	Asp	Arg	Trp	Asp	Leu	Pro	Leu		
281					880				885							890		
283	tca	gac	atg	tat	acc	ccg	tac	gtc	ttc	ccg	agc	gaa	aac	ggt	ctg	cgc	4180	
284	Ser	Asp	Met	Tyr	Thr	Pro	Tyr	Val	Phe	Pro	Ser	Glu	Asn	Gly	Leu	Arg		
285					895				900							905		
287	tgc	ggg	acg	cgct	gaa	ttt	aat	tat	ggc	cca	cac	cag	tgg	cgc	ggc	gac	4228	
288	Cys	Gly	Thr	Arg	Glu	Leu	Asn	Tyr	Gly	Pro	His	Gln	Trp	Arg	Gly	Asp		
289					910				915							920		
291	ttc	cag	ttc	acc	atc	agc	cgc	tac	agt	caa	cag	caa	ctg	atg	gaa	acc	4276	
292	Phe	Gln	Phe	Asn	Ile	Ser	Arg	Tyr	Ser	Gln	Gln	Gln	Leu	Met	Glu	Thr		
293	925					930					935						940	
295	agc	cat	cgct	cat	ctg	ctg	cac	gct	gaa	gaa	ggc	aca	tgg	ctg	aat	atc	4324	
296	Ser	His	Arg	His	Leu	Leu	His	Ala	Glu	Glu	Gly	Thr	Trp	Leu	Asn	Ile		
297					945				950							955		
299	gac	ggt	tcc	cat	atg	ggg	att	ggt	ggc	gac	gac	tcc	tgg	agc	ccg	tca	4372	
300	Asp	Gly	Phe	His	Met	Gly	Ile	Gly	Gly	Asp	Asp	Ser	Trp	Ser	Pro	Ser		
301					960				965							970		
303	gta	tcg	gct	gaa	ttc	cag	ctg	agc	gcc	ggt	cgc	tac	cat	tac	cag	ttt	4420	
304	Val	Ser	Ala	Glu	Phe	Gln	Leu	Ser	Ala	Gly	Arg	Tyr	His	Tyr	Gln	Leu		
305					975				980							985		
307	gtc	tgg	tgt	caa	aaa	aga	tct	gac	tat	aaa	gat	gag	gac	ctc	gac	cat	4468	
308	Val	Trp	Cys	Gln	Lys	Arg	Ser	Asp	Tyr	Lys	Asp	Glu	Asp	Leu	Asp	His		
309					990				995							1000		
311	cat	cat	cat	cat	cac	cgg	taataatagg	tagataagtg	actgattttaga								4516	
312	His	His	His	His	His	Arg												
313	1005					1010												
315	tgcatttgc	cctcgaccaa	ttccggttat	tttccaccat	attgccgtct	tttggcaatg	4576											

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L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

L:34 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1